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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=4; day=29; hr=15; min=19; sec=24; ms=251;]

=====

Reviewer Comments:

1.

E355 Empty lines found between the amino acid numbering and the proteins SEQID (22)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (22) POS (0)

<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide having Bam HI site

* * * * *

ggcggatccg tctcccagtt gttcttc

27

7

<210> 23

<211> 9

<212> DNA

<213> Helianthus annuus

Please remove the extra "7" between SEQ ID # 22 and SEQ ID # 23.

2.

E311 Invalid field content in <220> in SEQ ID (30)

E249 Order Sequence Error <223> -> ; Expected Mandatory Tag:
<400> in SEQID (30)

E250 Structural Validation Error; Sequence listing may not be

indexable

<210> 30

<211> 66

<212> PRT

<213> Artificial Sequence

<220> 30

<223> Synthetic fragment of Hahb-4

Ala	Glu	Lys	His	Gln	Glu	Lys	Thr	Ser	Ser	Ser	Gly	Ser	Gly	Glu	Glu
1				5				10					15		
Ser	Asp	Asp	Arg	Phe	Thr	Asn	Ser	Pro	Asp	Val	Met	Phe	Gly	Gln	Glu
			20					25					30		
Met	Asn	Val	Pro	Phe	Cys	Asp	Gly	Phe	Ala	Tyr	Phe	Glu	Glu	Gly	Asn
			35					40					45		
Ser	Leu	Leu	Glu	Ile	Glu	Glu	Gln	Leu	Pro	Asp	Pro	Gln	Lys	Trp	Trp
			50				55					60			
Glu	Phe														
65															

Numeric identifier <220> must remain blank. Please remove the number "30" from numeric identifier <220> in SEQ ID # 30. Numeric identifier <400> is mandatory. Please insert numeric identifier <400>, with the correct response, before the sequence in SEQ ID # 30.

3.

<110> Chan, Lia Raquel

Gonzalez, Daniel H.

Dezar, Carlos A.

Gago, Gabriela Marisa

Dunan, Claudio Marcelo

<120> Transcription Factor Gene Induced by Water Deficit Conditions and
Absciscic Acid from Helianthus Annuus, Promoter and Transgenic
Plants

<130> 2510.0040000/JAG/SAC

<140> 10/520,333

<141> 2003-05-02

<150> PCT/US2003/013770

<151> 2003-05-02

<160> 30

<170> PatentIn version 3.1

Numeric identifier <140> must contain the current application number.
Please change "10/520,333" to the correct application number "US
10/520,033."

4.

W213 Artificial or Unknown found in <213> in SEQ ID (4)

W213 Artificial or Unknown found in <213> in SEQ ID (5)

W213 Artificial or Unknown found in <213> in SEQ ID (6)

W213 Artificial or Unknown found in <213> in SEQ ID (7)

W213 Artificial or Unknown found in <213> in SEQ ID (8)

W213 Artificial or Unknown found in <213> in SEQ ID (9)

W213 Artificial or Unknown found in <213> in SEQ ID (11)

W213 Artificial or Unknown found in <213> in SEQ ID (12)

W213 Artificial or Unknown found in <213> in SEQ ID (13)

W213 Artificial or Unknown found in <213> in SEQ ID (14)

W213 Artificial or Unknown found in <213> in SEQ ID (15)

W213 Artificial or Unknown found in <213> in SEQ ID (16)

W213 Artificial or Unknown found in <213> in SEQ ID (17)

W213 Artificial or Unknown found in <213> in SEQ ID (18)

W213 Artificial or Unknown found in <213> in SEQ ID (19)

W213 Artificial or Unknown found in <213> in SEQ ID (20)

W213 Artificial or Unknown found in <213> in SEQ ID (21)

W213 Artificial or Unknown found in <213> in SEQ ID (22)

W213 Artificial or Unknown found in <213> in SEQ ID (25)

W213 Artificial or Unknown found in <213> in SEQ ID (26) This
error has occurred more than 20 times, will not be displayed

The warnings shown above are ok and require no response.

Application No: 10520033 Version No: 4.0

Input Set:

Output Set:

Started: 2009-04-29 14:31:05.500
Finished: 2009-04-29 14:31:07.691
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 191 ms
Total Warnings: 24
Total Errors: 5
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)

Input Set:

Output Set:

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26) This error has occurred more than 20 times, will not be displayed
E 311	Invalid field content in <220> in SEQ ID (30)
E 249	Order Sequence Error <223> -> ; Expected Mandatory Tag: <400> in SEQID (30)
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> Chan, Lia Raquel
Gonzalez, Daniel H.
Dezar, Carlos A.
Gago, Gabriela Marisa
Dunan, Claudio Marcelo

<120> Transcription Factor Gene Induced by Water Deficit Conditions and
Absciscic Acid from Helianthus Annuus, Promoter and Transgenic Plants

<130> 2510.0040000/JAG/SAC

<140> 10/520,333

<141> 2003-05-02

<150> PCT/US2003/013770

<151> 2003-05-02

<160> 30

<170> PatentIn version 3.1

<210> 1

<211> 774

<212> DNA

<213> Helianthus annuus

<400> 1

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aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga	180
cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg	240
gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat	300
aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag	360
aatcaggccc tactcaatca ggtatggttg caaacttaca atgttgcat caactattta	420
agtagttttg aatttttgtg acaataaaga ttgacaaatg ttgtttgata attgattaac	480
agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtggca	540
gcggtgaaga atcggtgat cggtttacga actctccgga cgttatgttt ggtcaagaaa	600
tgaatgttcc gttttgcgac ggttttgcgt actttgaaga aggaaacagt ttgttgagaga	660
ttgaagaaca actgccagac cctcaaaagt ggtgggagtt ctaaagagta aagaaggatg	720
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<210> 2
 <211> 673
 <212> DNA
 <213> *Helianthus annuus*

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aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga	180
cccgagttta ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg	240
gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat	300
aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag	360
aatcaggccc tactcaatca gttggaggtg ctgagaaatg tagcagaaaa gcatcaagag	420
aaaactagta gtagtggcag cggatgaaga tcggatgatc ggtttacgaa ctctccggac	480
gttatgtttg gtcaagaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa	540
ggaaacagtt tgttggagat tgaagaacaa ctgccagacc ctcaaaagtg gtgggagttc	600
taaagagtaa agaaggatgt agaagtagta gagtaaaaac taaaacatac cagatagttg	660
gtttacactt tgt	673

<210> 3
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 <212> DNA
 <213> *Helianthus annuus*

<220>
 <221> promoter
 <222> (1)..(1221)
 <223> Large allele

<400> 3

gatccaattg gaccacctgg cacatcgtag cttatctctt ttgtcgtttc caacacacca	60
caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc	120
atattaaaag tagtagcccc cccccatt tgtagctac catttccac tttaataatc	180
accacgcta tgtccacttg tacttttgtt tgcacacaac tcttccata aaatatcaaa	240
ccaaattttt tttagtggaa acaaatcc ccaaatagaa tactaacgaa attcatcgca	300
tcagaatata ctcatctctg aacagtggtg aagcttgacg ttttcgacgg ggggtcgga	360
aacgtatgta cccgaaattt ctatagaatc ggggggtcga aaacgtatat acccaaaatt	420

tctatacgaa aactacatat ataacactac tgagcaaaaa gttcgggggt tcgggcgccc	480
ctccccggccc cttcaaagct tcgccaatgt ctctgaaccg aagaaaaccc tcactcgtct	540
actagccaat gaatcctcac cagggaaacc ctactcgtc ttactggact attggcgctt	600
ccaaatggac tacttgcgaa attcaccaca tcgggatata ctcgtctact gcggtgaggt	660
aaaacccgct tggtcaagg atcgaaactag cgattgctgc ctactcgct aatctcccat	720
catcaacagg tgccgccgaa acaaaatgct gggggcggga gttgaacctt ggtccagtga	780
cgcacccatg aatttttttt ctagggatgc gaacgagtgg tttaaccata cttttaagag	840
gtgcgatcgg aaattttacc tataaaatac actaaaaaag ttccaagggt ccaccacccc	900
cttaacctaa gtccgccttt gtctggatca cgtgaaacat caggtctctc ccttaccagt	960
ccagctacga ctcatcgaca aaatatcaaa accatatgat tttagtttt atctcaaccg	1020
aaagtgcacat catgacagag aatcgacata accaaaacgt gtaaacgtac aactcaccat	1080
tgcgttgaaa aggacaaaac aggtaggatt cttgtcaaat tcaacgcgta cacctgtgct	1140
tcctctaaac cccatacttt aagaaccttt ataaagacca ctactatat atacacatat	1200
ataatatcac ttatcaaacc c	1221

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based on the promoter and having Hind I
II site

<400> 4

gcgaagcttg atgcgaacga gtggttta	28
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<210> 5

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based on the promoter and having Sal I
site

<400> 5

gcggtcgaca cctggcacat cgtatctt	28
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<210> 6

<211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Bam HI site

 <400> 6
 cgcggatccg agggtttgat aagtgat 27

 <210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Hind I II site

 <400> 7
 cccaagctta acctaagtcc gcctttg 27

 <210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Hind II I site

 <400> 8
 ggcaagctta tctcaaccga aagtgac 27

 <210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the 5' promoter

 <400> 9
 atttcgcaag tagtcatt 19

 <210> 10
 <211> 1015
 <212> DNA
 <213> Helianthus annuus

 <400> 10
 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca 60

caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc	120
atattaaaag tagtagcccc cccccccatt tgttacctac catttcccac ttttaataatc	180
accacacgta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa	240
ccaaattttt tttaatggaa aacaaatact tcaaatgcac tattggtgaa attcaccaca	300
tcagaatata cccgtctcta ctcatctact ggccaacgaa tcttcacggg ggaaaccctc	360
actcgtctac tgggactact ggcgcttcaa aatggactac tgacaaaatt caccacatcg	420
ggatacactt gtctactgcg gtgaggtaaa atccgcgct cagctcaatg atcgaactag	480
cgatcgccac ccactcacct tgtctcccat catcaccagg tgccgcaaaa acaaaatggt	540
gggggcgggga attgaacctt ggtccagtgg cgcacccatg aatttttttt ctagggatgc	600
gaacgagtga ttttaaccata cttttaagag gtgcgatcgg aaattttacc tataaaatat	660
actaaaaaaaa tttcaagggt cgcgccaccc accccttaac ctaagtccgc ctctgcctgg	720
atcacgtgaa acatcagggtc tctctcttac cagttcacct acaactcatt gacaaaatat	780
caaaaccata tgattttgag ttttatctca accgaaagtg acatcatgac agagaatcga	840
cataacccaaa acgtgtaaac gtacaactca ccattgcgtt gaaaaggaca aaacaggtag	900
gattcttgtc aaattcaacg cgtacacctg tgcttcatct aaacccata ctttaagaac	960
ctttataaag accactcact atatatacac atatataata tcacttatca aaccc	1015

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide that matches nucleotides 81-100 of the H
ahb-4 cDNA sequence and having Bam HI site

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ggcggatcca acagaaacaa ccaccagg	28
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<210> 12

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for cloning 5' cDNA and having Bam HI s
ite

<400> 12

ggcggatccc ctggtggttg tttctgttg	29
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<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide based on 5' cDNA and having Xho I site

 <400> 13
 gaggactcga gctcaagttt tttttttttt tttt 34

<210> 14
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide based on 5' cDNA and having Xho I site

 <400> 14
 gaggactcga gctcaagc 18

<210> 15
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Eco RI site

 <400> 15
 gccgaattca gattgagcaa gagtataac 29

<210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter

 <400> 16
 acctttataa agaccactc 19

<210> 17
 <211> 19
 <212> DNA
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<400> 17	
acgcaatggt gagttgtac	19
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<223> oligonucleotide to DNA-binding assays	
<400> 18	
aattcagatc tcaataattg agag	24
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gacacctca attattgaga tctg	24
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<212> DNA	
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gcgggatcca ccatgtctct tcaacaagta	30
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<400> 21	
gccgagctct tagaactcca accacttttg	30
<210> 22	
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<212> DNA	
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<220>

<223> Oligonucleotide having Bam HI site

<400> 22

ggcggatccg tctcccagtt gttcttc

27

7

<210> 23

<211> 9

<212> DNA

<213> Helianthus annuus

<220>

<221> misc_feature

<222> (5)..(5)

<223> n is a or t

<400> 23

caatnattg

9

<210> 24

<211> 181

<212> PRT

<213> Helianthus annuus

<400> 24

Met Ser Leu Gln Gln Val Pro Thr Thr Glu Thr Thr Thr Arg Lys Asn
1 5 10 15

Arg Asn Glu Gly Arg Lys Arg Phe Thr Asp Lys Gln Ile Ser Phe Leu
20 25 30

Glu Tyr Met Phe Glu Thr Gln Ser Arg Pro Glu Leu Arg Met Lys His
35 40 45

Gln Leu Ala His Lys Leu Gly Leu His Pro Arg Gln Val Ala Ile Trp
50 55 60

Phe Gln Asn Lys Arg Ala Arg Ser Lys Ser Arg Gln Ile Glu Gln Glu
65 70 75 80

Tyr Asn Ala Leu Lys His Asn Tyr Glu Thr Leu Ala Ser Lys Ser Glu
85 90 95

Ser Leu Lys Lys Glu Asn Gln Ala Leu Leu Asn Gln Leu Glu Val Leu

100

105

110

Arg Asn Val Ala Glu Lys His Gln Glu Lys Thr Ser Ser Ser Gly Ser
 115 120 125

Gly Glu Glu Ser Asp Asp Arg Phe Thr Asn Ser Pro Asp Val Met Phe
 130 135 140

Gly Gln Glu Met Asn Val Pro Phe Cys Asp Gly Phe Ala Tyr Phe Glu
 145 150 155 160

Glu Gly Asn Ser Leu Leu Glu Ile Glu Glu Gln Leu Pro Asp Pro Gln
 165 170 175

Lys Trp Trp Glu Phe
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<210> 25

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Hd-Zip domain of Athb-1

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 1 5 10 15

Glu Lys Ser Phe Glu Thr Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr
 20 25 30

Gln Leu Ala Lys Lys Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp
 35 40 45

Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Arg Asp
 50 55 60

Tyr Asp Leu Leu Lys Ser Thr Tyr Asp Gln Leu Leu Ser Asn Tyr Asp
 65 70 75 80

Ser Ile Val Met Asp Asn Asp Lys Leu Arg Ser Glu Val Thr Ser Leu
 85 90 95

Thr Glu Lys

<210> 26

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Hd-Zip domain of Athb-6

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1 5 10 15

Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Val
20 25 30

Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp
35 40 45

Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp
50 55 60

Tyr Gly Val Leu Lys Thr Gln Tyr Asp Ser Leu Arg His Asn Phe Asp
65 70 75 80

Ser Leu Arg Arg Asp Asn Glu Ser Leu Leu Gln Glu Ile Ser Lys Leu
85 90 95

Lys Thr Lys

<210> 27

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Hd-Zip domain of Athb-7

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Asn Lys Asn Asn Gln Arg Arg Phe Ser Asp Glu Gln Ile Lys Ser Leu
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Glu Met Met Phe Glu Ser Glu Thr Arg Leu Glu Pro Arg Lys Lys Val

20

25

30

Gln Leu Ala Arg Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Ile Trp
 35 40 45

Phe Gln Asn Lys Arg Ala Arg Trp Lys Ser Lys Gln Leu Glu Thr Glu
 50 55 60

Tyr Asn Ile Leu Arg Gln Asn Tyr Asp Asn Leu Ala Ser Gln Phe Glu
 65 70 75 80

Ser Leu Lys Lys Glu Lys Gln Ala Leu Val Ser Glu Leu Gln Arg Leu
 85 90 95

Lys Glu Ala

<210> 28

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Hd-Zip domain of Athb-12

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Glu Leu Ile Phe Glu Ser Glu Thr Arg Leu Glu Pro Arg Lys Lys Val
 20 25 30

Gln Val Ala Arg Glu Leu Gly Leu Gln Pro Arg Gln Met Thr Ile Trp
 35 40 45

Phe Gln Asn Lys Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Glu
 50 55 60

Tyr Asn Thr Leu Arg Ala Asn Tyr Asn Asn Leu Ala Ser Gln Phe Glu
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Ile Met Lys Lys Glu Lys Gln Ser Leu Val Ser Glu Leu Gln Arg Leu
 85 90 95

Asn Glu Glu

<210> 29

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Hd-Zip domain of Hahb-4

<400> 29

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1 5 10 15

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20 25 30

Gln Leu Ala His Lys Leu Gly Leu His Pro Arg Gln Val Ala Ile Trp
35 40 45

Phe Gln Asn Lys Arg Ala Arg Ser Lys Ser Arg Gln Ile Glu Gln Glu
50 55 60

Tyr Asn Ala Leu Lys His Asn Tyr Glu Thr Leu Ala Ser Lys Ser Glu
65 70 75 80

Ser Leu Lys Lys Glu Asn Gln Ala Leu Leu Asn Gln Leu Glu Val Leu
85 90 95

Arg Asn Val

<210> 30

<211> 66

<212> PRT

<213> Artificial Sequence

<220> 30

<223> Synthetic fragment of Hahb-4

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20 25 30

Met Asn Val Pro Phe Cys Asp Gly Phe Ala Tyr Phe Glu Glu Gly Asn
35 40 45

Ser Leu Leu Glu Ile Glu Glu Gln Leu Pro Asp Pro Gln Lys Trp Trp
50 55 60

Glu Phe
65